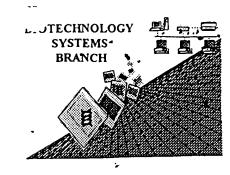BᵢₒTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _4/06/04 02/977,283_

Source: _OIPE_

Date Processed by STIC: _11/06/01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov **or phone 703-306-4119 (R. Wax)**
PATENTIN 3.0 e-mail help: patin3help@uspto.gov **or phone 703-306-4119 (R. Wax)**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 11/06/01

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

1_____Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino Numbering — The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length. — Sequence(s)_____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)_____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7_____Skipped Sequences (OLD RULES) — Sequence(s)_____ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences (NEW RULES) — Sequence(s)_____ missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10_____Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown is Artificial Sequence

11_____Use of <220> — Sequence(s)_____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n — n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MII – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING   DATE: 11/06/2001
PATENT APPLICATION: US/09/977,283   TIME: 12:08:08

Input Set : **A:\Sequence listing ascii**
Output Set: **N:\CRF3\11062001\I977283.raw**

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     9  <120> TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis
    13  <130> FILE REFERENCE: 0609.4320003
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C-->19  <141> CURRENT FILING DATE: 2001-10-16
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    78  <212> TYPE: PRT
    80  <213> ORGANISM: Artificial Sequence
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    86  <223> OTHER INFORMATION: Alpha-2 Antiplasmin Antibody
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   104  <220> FEATURE:
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   114  <223> OTHER INFORMATION: May be any Amino Acid
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Does Not Comply
Corrected Diskette Needed

See page 2 of 7

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152 <222> LOCATION: (1)..(60)
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161 -20             -15             -10                     -5
163 ggt gcc aga tgt gac atc cag atg act cag tct cca gcc tcc cta tct    96
164 Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
165                      1               5                   10
167 gca tct gtg gga gaa act gtc acc atc aca tgt cga gca agt ggg aat   144
168 Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn
169         15                  20                  25
171 att cac aat tat tta gca tgg tat cag cag aaa cag gga aaa tct cct   192
172 Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
173         30                  35                  40
175 cag ctc ctg gtc tat aat gca aaa acc tta gca gat ggt gtg cca tca   240
176 Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser
177  45                 50                  55                  60
179 agg ttc agt ggc agt gga tca gga aca caa ttt tct ctc agg atc aac   288
180 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Arg Ile Asn
181                 65                  70                  75
183 agc ctg cag cct gaa gat ttt ggg agt cat tac tgt caa cat ttt tgg   336
184 Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp
185                 80                  85                  90
187 acc act ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa       381
188 Thr Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
189         95                  100                 105
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208 <223> OTHER INFORMATION: May be either Gly or Ala
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W--> (handwritten annotations) Errored: Xaa should be explained in

Does Not Comply
Corrected Diskette Needed

Does Not Comply
Corrected Diskette Needed

good

RAW SEQUENCE LISTING   DATE: 11/06/2001
PATENT APPLICATION: US/09/977,283   TIME: 12:08:08

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Output Set: N:\CRF3\11062001\I977283.raw

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     221               1               5               10
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     225          15              20              25
     228 Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
     229      30              35              40
     232 Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser
     233  45              50              55                      60
     236 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Arg Ile Asn
     237              65              70                      75
     240 Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp
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     266 <222> LOCATION: (1)..(381)
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     289               1               5               10
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     292 Ala Ser Val Gly Glu Thr Val Thr Val Thr Cys Arg Ala Ser Gly Asn
     293          15              20              25
     295 att cac aat tat tta gca tgg tat cag cag aaa cag gga aaa tct cct      192
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     297      30              35              40
     299 cag ctc ctg gtc tat aat gca aga acc tta gca gat ggt gtg cca tca      240
     300 Gln Leu Leu Val Tyr Asn Ala Arg Thr Leu Ala Asp Gly Val Pro Ser
     301  45              50              55                      60
     303 agg ttc agt ggc agt gga tca gga aca caa tat tct ctc aag atc aac      288
     304 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn
     305              65              70                      75
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307 agc ctg cag cct gaa gat ttt ggg agt tat tac tgt caa cat ttt tgg     336
308 Ser Leu Gln Pro Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp
309             80                85                90
311 agt aat ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa         381
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337                 1                 5                 10
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341         15                20                25
344 Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
345         30                35                40
348 Gln Leu Leu Val Tyr Asn Ala Arg Thr Leu Ala Asp Gly Val Pro Ser
349 45                50                55                60
352 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn
353                 65                70                75
356 Ser Leu Gln Pro Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp
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401 -20                 -15                 -10                 -5
403 ggt gcc aga tgt gac atc cag atg act cag tct cca gcc tcc cta tct     96
404 Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
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405                  1            5                  10
407 gca tct gtg gga gaa act gtc acc atc aca tgt cga gca agt ggg aat      144
408 Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn
409          15                  20                  25
411 att cac aat tat tta gca tgg tat cag cag aaa cag gga aaa tct cct      192
412 Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
413          30                  35              40
415 caa ctc ctg gtc tat aat gca aaa acc tta gca gat ggt gtg cca tca      240
416 Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser
417   45                  50                  55              60
419 agg ttc agt ggc agt gga tca gga aca caa ttt tct ctc aag atc aac      288
420 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn
421              65                  70                  75
423 agc ctg cag cct gaa gat ttt ggg agt cat tac tgt caa cat ttt tgg      336
424 Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp
425          80                  85                  90
427 acc act ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa        381
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457          15                  20                  25
460 Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
461          30                  35              40
464 Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser
465   45                  50                  55              60
468 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn
469              65                  70                  75
472 Ser Leu Gln Pro Glu Asp Phe Gly Ser His Tyr Cys Gln His Phe Trp
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VERIFICATION SUMMARY   DATE: 11/06/2001
PATENT APPLICATION: **US/09/977,283**   TIME: 12:08:09

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L:19   M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:70   M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:120  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:160  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
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